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 START SED IDW 2
 GTTGGTCTCCTGCCGTGCCCGGAATCCAGTCAGAAGTTCCAGCCTGCCACTGTTCTCTGATGCCATG CCA GCA 3
 START SED IDW 3
 P T Q L F F P L I R N C E L S R I Y G T 23
 CCA ACT CAA CTG TTT TTT CCT CTC ATC CGT AAC TGT GAA CTG AGC AGG ATC TAT GGC ACT 69
 A C Y C H H K H L C C S S S Y I P Q S R 43
 GCA TGT TAC TGC CAC CAC AAA CAT CTC TGT TGT TCC TCA TCG TAC ATT CCT CAG AGT CGA 129
 L R Y T P H P A Y A T F C R P K E N W W 63
 CTG AGA TAC ACA CCT CAT CCA GCA TAT GCT ACC TTT TGC AGG CCA AAG GAG AAC TGG TGG 189
 Q Y T Q G R R Y A S T P Q K F Y L T P P 83
 CAG TAC ACC CAA GGA AGG AGA TAT GCT TCC ACA CCA CAG AAA TTT TAC CTC ACA CCT CCA 249
 Q V N S I L K A N E Y S F K V P E F D G 103
 CAA GTC AAT AGC ATC CTT AAA GCT AAT GAA TAC AGT TTC AAA GTG CCA GAA TTT GAC GGC 309
 K N V S S I L G F D S N Q L P A N A P I 123
 AAA AAT GTC AGT TCT ATC CTT GGA TTT GAC AGC AAT CAG CTG CCT GCA AAT GCA CCC ATT 369
 E D R R S A A T C L Q T R G M L L G V F 143
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 D G H A G C A C S Q A V S E R L F Y Y I 163
 GAT GGC CAT GCA GGT TGT GCT TGT TCC CAG GCA GTC AGT GAA AGA CTC TTT TAT TAT ATT 489
 A V S L L P H E T L L E I E N A V E S G 183
 GCT GTC TCT TTG TTA CCC CAT GAG ACT TTG CTA GAG ATT GAA AAT GCA GTG GAG AGC GGC 549
 R A L L P I L Q W H K H P N D Y F S K E 203
 CGG GCA CTG CTA CCC ATT CTC CAG TGG CAC AAG CAC CCC AAT GAT TAC TTT AGT AAG GAG 609
 A S K L Y F N S L R T Y W Q E L I D L N 223
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 T G E S T D I D V K E A L I N A F K R L 243
 ACT GGT GAG TCG ACT GAT ATT GAT GTT AAG GAG GCT CTA ATT AAT GCC TTC AAG AGG CTT 729
 D N D I S L E A Q V G D P N S F L N Y L 263
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 V L R V A F S G A T A C V A H V D G V D 283
 GTG CTT CGA GTG GCA TTT TCT GGA GCC ACT GCT TGT GTG GCC CAT GTG GAT GGT GTT GAC 849
 L H V A N T G D S R A M L G V Q E E D G 303
 CTT CAT GTG GCC AAT ACT GGC GAT AGC AGA GCC ATG CTG GGT GTG CAG GAA GAG GAC GGC 909

Figure 1A

S W S A V T L S N D H N A Q N E R E L E 323
 TCA TGG TCA GCA GTC ACG CTG TCT AAT GAC CAC AAT GCT CAA AAT GAA AGA GAA CTA GAA 969

 R L K L E H P K S E A K S V V K Q D R L 343
 CGG CTG AAA TTG GAA CAT CCA AAG AGT GAG GCC AAG AGT GTC GTG AAA CAG GAT CGG CTG 1029

 L G L L M P F R A F G D V K F K W S I D 363
 CTT GGC TTG CTG ATG CCA TTT AGG GCA TTT GGA GAT GTA AAG TTC AAA TGG AGC ATT GAC 1089

 L Q K R V I E S G P D Q L N D N E Y T K 383
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 F I P P N Y H T P P Y L T A E P E V T Y 403
 TTT ATT CCT CCT AAT TAT CAC ACA CCT CCT TAT CTC ACT GCT GAG CCA GAG GTA ACT TAC 1209

 H R L R P Q D K F L V L A T D G L W E T 423
 CAC CGA TTA AGG CCA CAG GAT AAG TTT CTG GTG TTG GCT ACT GAT GGG TTG TGG GAG ACT 1269

 M H R Q D V V R I V G E Y L T G M H H Q 443
 ATG CAT AGG CAG GAT GTG GTT AGG ATT GTG GGT GAG TAC CTA ACT GGC ATG CAT CAC CAA 1329

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 R H A V G N N E F G T V D H E R L S K M 503
 CGC CAC GCT GTG GGC AAC AAC GAG TTT GGG ACT GTT GAT CAT GAG CGC CTC TCT AAA ATG 1509

 L S L P E E L A R M Y R D D I T I I V V 523
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End of seq IDNO: 2
 End of seq IDNO: 3
 End of seq IDNO: 1

Figure 1.B

Analysis of 26583 (537 aa)

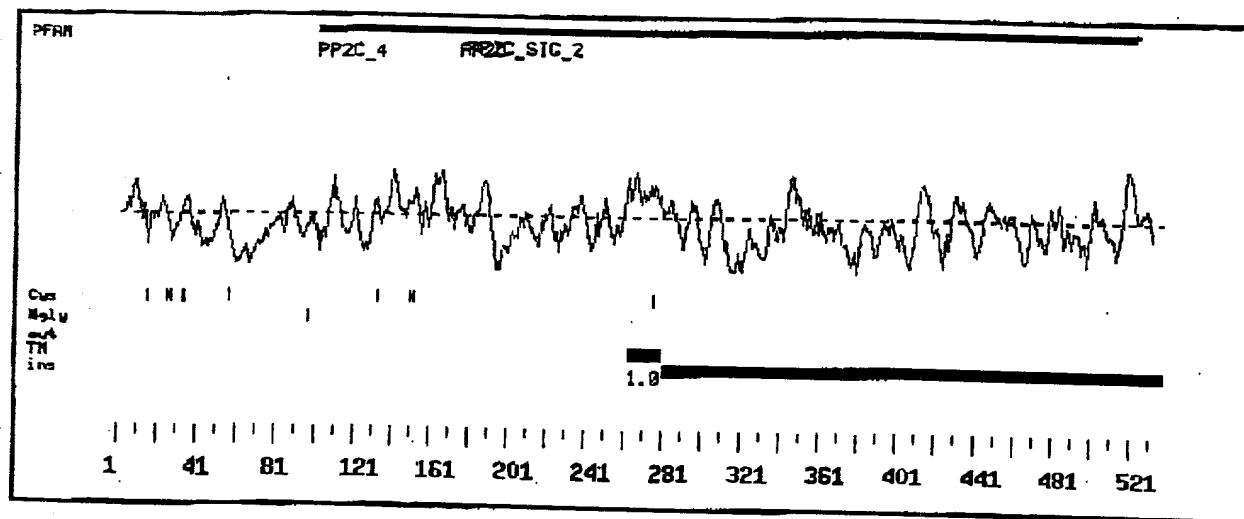


Figure 2

PP2C: domain 1 of 1, from 173 to 461: score 261.3, E = 1.3e-74

26583 173 LLEIENAVESGRALLPILQWHKHPNDYF-SKEASKLYFNSLRTYWQE 218 SEQ ID NO:4
 26583 173 LLEIENAVESGRALLPILQWHKHPNDYF-SKEASKLYFNSLRTYWQE 218 SEQ ID NO:2

26583 219 LIDLNTGESTDIDVKEALINAFKRLDN-----DISLEAQVGDPSFLNY 262

26583 263 LVLRL-----VAFSGATACVAHVVDGVDLHVANTGDSRAHLGVQ 299

26583 300 EEDGSWAVTSLNDHNAQNERELERLKLHPKSEAKSVVKQDRLLGLLMP 349

26583 350 FRAFGDVKFKWSIDLQKRVIESGPDQLNDNXTKFIpphyhtpPYLTAEP 399

26583 400 EVT-YHRLRPQ-DKFLVLATDGLWETHRQDVVRIVGEYLTGM-----H 461

26583 442 HQQPIAVGGYKVTLCQMHGL 461

Figure 3A

00001257-030601

PF2C_4: domain 1 of 1, from 99 to 523; score 338.5, E = 7.6e-98

```

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26583 99 PFIDGKNVSSILGF-DSNQLPANAPIEDRRSAATclqtrgmLLGVFD 144
                                     SEQ ID NO:5
                                     SEQ ID NO:2
                                     GHGGseaaakflskniheilaeeelsfdkdeslkene.e.lk.d.ep.....
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26583 145 GHACCACSQAVSERLFYYIAVSLLPHETLLEIENAVsGRaLlPllqwhk 194
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+++ ++ ++ ++ +++++ +ln+g+++ dv+aal++sF+r+d
26583 195 hndyfskeasklyfnslrTYWqElIdLntGcESTDIDVKEALINAFKRLD 244
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++i+ + + +++++ + + + +TA+va++g +l+vAN+GDSRa
26583 245 NDIslleaqvqdpnsflnylvlrvaFsgATACVAHVdGVdLHVANTGDSRa 294
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26583 295 MLGVQEEDqSW-----SAVTLSDHNAQNERELERLKLEMPKSE--AKS 336
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26583 337 VVKQD-----RLGL---LMPFRAFgDVKFKwsIDLqKrVIEsgpdqLNd 378
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26583 379 NEYTKFIPPNYHTFPYLTAEPVTYHRL-----RPQDKFLVLATDGLWE 422
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+ q++v iv + l+++++++ +++++ +++++ +++++ +
26583 423 TTHRQDVVRIVGEYLTGHHQqPIAVGCYKVTlGgmHClteRrtkmsav 472
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++++ ++l R+ +++++ ++L +++ ++ + +D+it++v
26583 473 fedqnaethliRhaVGNNEFGTVdHERLSqLslpeelarmyRDOITITV 522
                                     v<-
                                     v
26583 523 V 523

```

Figure 3B

